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RAW SEQUENCE LISTING

DATE: 08/02/2004

PATENT APPLICATION: US/10/801,847

TIME: 14:48:35

Input Set : N:\Crf3\RULE60\10801847.raw

Output Set: N:\CRF4\08022004\J801847.raw

1 <110> APPLICANT: HERMANN, Thomas
 2 WOLF, Andreas
 3 MORBACH, Susanne
 4 KRAMER, Reinhard
 5 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE OtsA PROTEIN
 6 <130> FILE REFERENCE: 215482USOX
 7 <140> CURRENT APPLICATION NUMBER: US/10/801,847
 8 <141> CURRENT FILING DATE: 2004-03-17
 9 <150> PRIOR APPLICATION NUMBER: US/10/058,945
 10 <151> PRIOR FILING DATE: 2002-01-30
 11 <150> PRIOR APPLICATION NUMBER: DE 10103873.9
 12 <151> PRIOR FILING DATE: 2001-01-30
 13 <150> PRIOR APPLICATION NUMBER: DE 10110760.9
 14 <151> PRIOR FILING DATE: 2000-03-07
 15 <160> NUMBER OF SEQ ID NOS: 4
 16 <170> SOFTWARE: PatentIn version 3.1
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 3010
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Corynebacterium glutamicum
 22 <220> FEATURE:
 23 <221> NAME/KEY: CDS
 24 <222> LOCATION: (884)..(2338)
 25 <223> OTHER INFORMATION:

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 29 gcccgtcgat tcttgattcc accggtgatt gtggcgattg ccggcatcac accaatgctt 180
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 32 ggtgagtgga ttgccgcag gctacgtcgt ccaccacgct tcaaccata ccgtgcattt 360
 33 accaaggcga atgagttctc cttccaggag gaagctgagc agaatcagcg ccggcagaga 420
 34 aaacgtccaa agactaatca gagattcggg aataaaaagg aaaaatcaac ctgcttaggc 480
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 41 caccgcaaag aagaccacaa agaagtctta agccggatct tat atg gat gat tcc 895
 42 Met Asp Asp Ser
 43 1
 44 aat agc ttt gta gtt gtt gct aac cgt ctg cca gtg gat atg act gtc 943

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46	5 10 15 20	
47	cac cca gat ggt agc tat agc atc tcc ccc agc ccc ggt ggc ctt gtc	991
48	His Pro Asp Gly Ser Tyr Ser Ile Ser Pro Ser Pro Gly Gly Leu Val	
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50	acg ggg ctt tcc ccc gtt ctg gaa caa cat cgt gga tgt tgg gtc gga	1039
51	Thr Gly Leu Ser Pro Val Leu Glu Gln His Arg Gly Cys Trp Val Gly	
52	40 45 50	
53	tgg cct gga act gta gat gtt gca ccc gaa cca ttt cga aca gat acg	1087
54	Trp Pro Gly Thr Val Asp Val Ala Pro Glu Pro Phe Arg Thr Asp Thr	
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56	ggt gtt ttg ctg cac cct gtt gtc ctc act gca agt gac tat gaa ggc	1135
57	Gly Val Leu Leu His Pro Val Val Leu Thr Ala Ser Asp Tyr Glu Gly	
58	70 75 80	
59	ttc tac gag ggc ttt tca aac gca acg ctg tgg cct ctt ttc cac gat	1183
60	Phe Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro Leu Phe His Asp	
61	85 90 95 100	
62	ctg att gtt act ccg gtg tac aac acc gat tgg tgg cat gcg ttt cgg	1231
63	Leu Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp His Ala Phe Arg	
64	105 110 115	
65	gag gta aac ctc aag ttc gct gaa gcc gtg agc caa gtg gcg gca cac	1279
66	Glu Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln Val Ala Ala His	
67	120 125 130	
68	ggt gcc act gtg tgg gtg cag gac tat cag ctg ttg ctg gtt cct ggc	1327
69	Gly Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu Leu Val Pro Gly	
70	135 140 145	
71	att ttg cgc cag atg cgc cct gat ttg aag atc ggt ttc ttc ctc cac	1375
72	Ile Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly Phe Phe Leu His	
73	150 155 160	
74	att ccc ttc cct tcc cct gat ctg ttc cgt cag ctg ccg tgg cgt gaa	1423
75	Ile Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu Pro Trp Arg Glu	
76	165 170 175 180	
77	gag att gtt cga ggc atg ctg ggc gca gat ttg gtg gga ttc cat ttg	1471
78	Glu Ile Val Arg Gly Met Leu Gly Ala Asp Leu Val Gly Phe His Leu	
79	185 190 195	
80	gtt caa aac gca gaa aac ttc ctt gcg tta acc cag cag gtt gcc ggc	1519
81	Val Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr Gln Gln Val Ala Gly	
82	200 205 210	
83	act gcc ggg tct cat gtg ggt cag ccg gac acc ttg cag gtc agt ggt	1567
84	Thr Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu Gln Val Ser Gly	
85	215 220 225	
86	gaa gca ttg gtg cgt gag att ggc gct cat gtt gaa acc gct gac gga	1615
87	Glu Ala Leu Val Arg Glu Ile Gly Ala His Val Glu Thr Ala Asp Gly	
88	230 235 240	
89	agg cga gtt agc gtc ggg gcg ttc ccg atc tcg att gat gtt gaa atg	1663
90	Arg Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile Asp Val Glu Met	
91	245 250 255 260	
92	ttt ggg gag gcg tcg aaa agc gcc gtt ctt gat ctt tta aaa acg ctc	1711
93	Phe Gly Glu Ala Ser Lys Ser Ala Val Leu Asp Leu Leu Lys Thr Leu	

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96	Asp Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg Leu Asp Tyr Thr						
97		280		285		290	
98	aag ggc att ttg cag cgc ctg ctt gcg ttt gag gaa ctg ctg gaa tcc						1807
99	Lys Gly Ile Leu Gln Arg Leu Leu Ala Phe Glu Glu Leu Leu Ser						
100		295		300		305	
101	ggc gcg ttg gag gcc gac aaa gct gtg ttg ctg cag gtc gcg acg cct						1855
102	Gly Ala Leu Glu Ala Asp Lys Ala Val Leu Leu Gln Val Ala Thr Pro						
103		310		315		320	
104	tcg cgt gag cgc att gat cac tat cgt gtg tcg cgt tcg cag gtc gag						1903
105	Ser Arg Glu Arg Ile Asp His Tyr Arg Val Ser Arg Ser Gln Val Glu						
106		325		330		335	340
107	gaa gcc gtc ggc cgt atc aat ggt cgt ttc ggt cgc atg ggg cgt ccc						1951
108	Glu Ala Val Gly Arg Ile Asn Gly Arg Phe Gly Arg Met Gly Arg Pro						
109		345		350		355	
110	gtg gtg cat tat cta cac agg tca ttg agc aaa aat gat ctc cag gtg						1999
111	Val Val His Tyr Leu His Arg Ser Leu Ser Lys Asn Asp Leu Gln Val						
112		360		365		370	
113	ctg tat acc gca gcc gat gtc atg ctg gtt acg cct ttt aaa gac ggt						2047
114	Leu Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro Phe Lys Asp Gly						
115		375		380		385	
116	atg aac ttg gtg gct aaa gaa ttc gtg gcc aac cac cgc gac ggc act						2095
117	Met Asn Leu Val Ala Lys Glu Phe Val Ala Asn His Arg Asp Gly Thr						
118		390		395		400	
119	ggt gct ttg gtg ctg tcc gaa ttt gcc ggc gcg gcc act gag ctg acc						2143
120	Gly Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala Thr Glu Leu Thr						
121		405		410		415	420
122	ggt gcg tat tta tgc aac cca ttt gat gtg gaa tcc atc aaa cgg caa						2191
123	Gly Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser Ile Lys Arg Gln						
124		425		430		435	
125	atg gtg gca gct gtc cat gat ttg aag cac aat ccg gaa tct gcg gca						2239
126	Met Val Ala Ala Val His Asp Leu Lys His Asn Pro Glu Ser Ala Ala						
127		440		445		450	
128	acg cga atg aaa acg aac agc gag cag gtc tat acc cac gac gtc aac						2287
129	Thr Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr His Asp Val Asn						
130		455		460		465	
131	gtg tgg gct aat agt ttc ctg gat tgt ttg gca cag tcg gga gaa aac						2335
132	Val Trp Ala Asn Ser Phe Leu Asp Cys Leu Ala Gln Ser Gly Glu Asn						
133		470		475		480	
134	tca tgaaccgcgc acgaatcgcg accataggcg ttcttccgct tgctttactg						2388
135	Ser						
136	485						
137	ctggcgctcct gtgggttcaga caccgtggaa atgacagatt ccacctgggt ggtgaccaat						2448
138	atttacaccg atccagatga gtccaattcg atcagtaatc ttgtcatttc ccagcccagc						2508
139	ttagattttg gcaattcttc cctgtctggt ttcactggct gtgtgccttt tacggggcgt						2568
140	gcggaattct tccaaaatgg tgagcaaagc tctgttcttg atgccgatta tgtgacctg						2628
141	tcttccctgg atttcgataa acttcccgat gattgccaaag gacaagaact caaagttcat						2688
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145      acactggttc ccatgacttt gactattgag gaaatcgcca agacaaaaaa gcttttggtt      2928
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157      20          25          30
158      Gly Gly Leu Val Thr Gly Leu Ser Pro Val Leu Glu Gln His Arg Gly
159      35          40          45
160      Cys Trp Val Gly Trp Pro Gly Thr Val Asp Val Ala Pro Glu Pro Phe
161      50          55          60
162      Arg Thr Asp Thr Gly Val Leu Leu His Pro Val Val Leu Thr Ala Ser
163      65          70          75          80
164      Asp Tyr Glu Gly Phe Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro
165      85          90          95
166      Leu Phe His Asp Leu Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp
167      100         105         110
168      His Ala Phe Arg Glu Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln
169      115         120         125
170      Val Ala Ala His Gly Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu
171      130         135         140
172      Leu Val Pro Gly Ile Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly
173      145         150         155         160
174      Phe Phe Leu His Ile Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu
175      165         170         175
176      Pro Trp Arg Glu Glu Ile Val Arg Gly Met Leu Gly Ala Asp Leu Val
177      180         185         190
178      Gly Phe His Leu Val Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr Gln
179      195         200         205
180      Gln Val Ala Gly Thr Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu
181      210         215         220
182      Gln Val Ser Gly Glu Ala Leu Val Arg Glu Ile Gly Ala His Val Glu
183      225         230         235         240
184      Thr Ala Asp Gly Arg Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile
185      245         250         255
186      Asp Val Glu Met Phe Gly Glu Ala Ser Lys Ser Ala Val Leu Asp Leu
187      260         265         270
188      Leu Lys Thr Leu Asp Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg
189      275         280         285
190      Leu Asp Tyr Thr Lys Gly Ile Leu Gln Arg Leu Leu Ala Phe Glu Glu
191      290         295         300
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193      305      310      315      320
194 Val Ala Thr Pro Ser Arg Glu Arg Ile Asp His Tyr Arg Val Ser Arg
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197      340      345      350
198 Met Gly Arg Pro Val Val His Tyr Leu His Arg Ser Leu Ser Lys Asn
199      355      360      365
200 Asp Leu Gln Val Leu Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro
201      370      375      380
202 Phe Lys Asp Gly Met Asn Leu Val Ala Lys Glu Phe Val Ala Asn His
203      385      390      395      400
204 Arg Asp Gly Thr Gly Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala
205      405      410      415
206 Thr Glu Leu Thr Gly Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser
207      420      425      430
208 Ile Lys Arg Gln Met Val Ala Ala Val His Asp Leu Lys His Asn Pro
209      435      440      445
210 Glu Ser Ala Ala Thr Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr
211      450      455      460
212 His Asp Val Asn Val Trp Ala Asn Ser Phe Leu Asp Cys Leu Ala Gln
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227 <213> ORGANISM: Corynebacterium glutamicum
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VERIFICATION SUMMARY

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